SEQUENCE LISTING

<110> SmithLine Beecham Biologicals S.A.

<120> Novel Compounds

<130> BC45203

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 1106
<212> DNA
<213> Homo Sapiens

<400> 1

```
tcgggttccg cagatgcaga ggttgaggtg gctgcgggac tggaagtcat cgggcagagg      60
tctcacagca gccaaggaac ctggggcccg ctcctccccc ctccaggcca tgaggattct     120
gcagttaatc ctgcttgctc tggcaacagg gcttgtaggg ggagagacca ggatcatcaa     180
ggggttcgag tgcaagcctc actcccagcc ctggcaggca gccctgttcg agaagacgcg     240
gctactctgt ggggcgacgc tcatcgcccc cagatggctc ctgacagcag cccactgcct     300
caagccccgc tacatagttc acctggggca gcacaacctc cagaaggagg agggctgtga     360
gcagacccgg acagccactg agtccttccc ccaccccggc ttcaacaaca gcctccccaa     420
caaagaccac cgcaatgaca tcatgctggt gaagatggca tcgccagtct ccatcacctg     480
ggctgtgcga cccctcaccc tctcctcacg ctgtgtcact gctggcacca gctgcctcat     540
ttccggctgg ggcagcacgt ccagccccca gttacgcctg cctcacacct tgcgatgcgc     600
caacatcacc atcattgagc accagaagtg tgagaacgcc taccccggca acatcacaga     660
caccatggtg tgtgccagcg tgcaggaagg gggcaaggac tcctgccagg gtgactccgg     720
gggccctctg gtctgtaacc agtctcttca aggcattatc tcctggggcc aggatccgtg     780
tgcgatcacc cgaaagcctg gtgtctacac gaaagtctgc aaatatgtgg actggatcca     840
ggagacgatg aagaacaatt agactggacc cacccaccac agcccatcac cctccatttc     900
cacttggtgt ttggttcctg ttcactctgt taataagaaa ccctaagcca agaccctcta     960
cgaacattct ttgggcctcc tggactacag gagatgctgt cacttaataa tcaacctggg    1020
gttcgaaatc agtgagacct ggattcaaat tctgccttga aatattgtga ctctgggaat    1080
gacaacacct ggtttgttct ctgttg                                         1106
```

<210> 2
<211> 282

```
<212> PRT
<213> homo sapiens


<400> 2
Met Gln Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly
 1               5                   10                  15
Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala
                20                  25                  30
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
            35                  40                  45
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
        50                  55                  60
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
65                  70                  75                  80
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
                85                  90                  95
Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
                100                 105                 110
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
        115                 120                 125
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
        130                 135                 140
Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
145                 150                 155                 160
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
                165                 170                 175
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
                180                 185                 190
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
            195                 200                 205
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
        210                 215                 220
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
225                 230                 235                 240
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
                245                 250                 255
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
                260                 265                 270
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
        275                 280


<210> 3
```

<211> 1158

<212> DNA

<213> homo sapiens

5   <400> 3

```
ggcacgaggg aaagccaagg gaagggacct aactgaaaac aaacaagctg ggagaagcag      60
gaatctgcgc tcgggttccg cagatgcaga ggttgaggtg gctgcgggac tggaagtcat     120
cgggcagagg tctcacagca gccaaggaac ctggggcccg ctcctccccc ctccaggcca     180
tgaggattct gcagttaatc ctgcttgctc tggcaacagg gcttgtaggg ggagagacca     240
ggatcatcaa ggggttcgag tgcaagcctc actcccagcc ctggcaggca gccctgttcg     300
agaagacgcg gctactctgt ggggcgacgc tcatcgcccc cagatggctc ctgacagcag     360
cccactgcct caagccccgc tacatagttc acctggggca gcacaacctc agaaggagg      420
agggctgtga gcagacccgg acagccactg agtccttccc caccccggc  ttcaacaaca     480
gcctccccaa caaagaccac cgcaatgaca tcatgctggt gaagatggca tcgccagtct     540
ccatcacctg ggctgtgcga cccctcaccc tctcctcacg ctgtgtcact gctggcacca     600
gctgcctcat ttccggctgg ggcagcacgt ccagccccca gttacgcctg cctcacacct     660
tgcgatgcgc caacatcacc atcattgagc accagaagtg tgagaacgcc tacccccggca     720
acatcacaga caccatggtg tgtgccagcg tgcaggaagg gggcaaggac tcctgccagg     780
gtgactccgg gggccctctg tctgtaacc agtctcttca aggcattatc tcctggggcc      840
aggatccgtg tgcgatcacc cgaaagcctg tgtctacac  gaaagtctgc aaatatgtgg      900
actggatcca ggagacgatg aagaacaatt agactggacc cacccaccac agcccatcac     960
cctccatttc cacttggtgt ttggttcctg ttcactctgt taataagaaa ccctaagcca    1020
agaccctcta cgaacattct ttgggcctcc tggactacag gagatgctgt cacttaataa    1080
tcaacctggg gttcgaaatc agtgagacct ggattcaaat tctgccttga aatattgtga    1140
ctctgggaat gacaacac                                                  1158
```

<210> 4

<211> 281

<212> PRT

<213> homo sapiens

<400> 4

```
Met Gln Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly
1               5                   10                  15
Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala
            20                  25                  30
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
        35                  40                  45
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
    50                  55                  60
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
65                  70                  75                  80
```

```
        Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
                         85                  90                  95
        Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
                        100                 105                 110
  5     Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
                    115                 120                 125
        Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
                130                 135                 140
        Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
 10     145                 150                 155                 160
        Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
                        165                 170                 175
        Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
                        180                 185                 190
 15     Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
                        195                 200                 205
        Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
                        210                 215                 220
        Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 20     225                 230                 235                 240
        Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
                        245                 250                 255
        Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
                        260                 265                 270
 25     Asp Trp Ile Gln Glu Thr Met Lys Asn
                        275                 280
```

SEQUENCE INFORMATION

SEQ ID NO:1

TCGGGTTCCGCAGatgcagaggttgaggtggctgcgggactggaagtcatcgggcagaggtctcacagcagccaa
ggaacctggggcccgctcctcccccctccaggccatgaggattctgcagttaatcctgcttgctctggcaacagggcttgtaggg
ggagagaccaggatcatcaaggggttcgagtgcaagcctcactcccagccctggcaggcagccctgttcgagaagacgcg
gctactctgtggggcgacgctcatcgcccccagatggctcctgacagcagcccactgcctcaagccccgctacatagttc
acctggggcagcacaacctccagaaggaggagggctgtgagcagacccggacagccactgagtccttcccccaccccggc
ttcaacaacagcctccccaacaaagaccaccgcaatgacatcatgctggtgaagatggcatcgccagtctccatcacctg
ggctgtgcgacccctcaccctctcctcacgctgtgtcactgctggcaccagctgcctcatttccggctggggcagcacgt
ccagccccccagttacgcctgcctcacaccttgcgatgcgccaacatcaccatcattgagcaccagaagtgtgagaacgcc
taccccggcaacatcacagacaccatggtgtgtgccagcgtgcaggaagggggcaaggactcctgccagggtgactccgg
gggccctctggtctgtaaccagtctcttcaaggcattatctcctggggccaggatccgtgtgcgatcacccgaaagcctg
gtgtctacacgaaagtctgcaaatatgtggactggatccaggagacgatgaagaacaattagACTGGACCCACCCA
CCACAGCCCATCACCCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGT
TAATAAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGG
ACTACAGGAGATGCTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGA
GACCTGGATTCAAATTCTGCCTTGAAATATTGTGACTCTGGGAATGACAACAC
CTGGTTTGTTCTCTGTTG

SEQ ID NO:2

MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAMRILQLILLALATGLVGGETRII
KGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNL
QKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAVRPLTLS
SRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTMVC
ASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVD
WIQETMKNN

SEQ ID NO:3

GGCACGAGGGAAAGCCAAGGGAAGGGACCTAACTGAAAACAAACAAGCTGG
GAGAAGCAGGAATCTGCGCTCGGGTTCCGCAGATGCAGAGGTTGAGGTGGCT
GCGGGACTGGAAGTCATCGGGCAGAGGTCTCACAGCAGCCAAGGAACCTGG
GGCCCGCTCCTCCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATCCTGCTTG
CTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGA
GTGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTCGAGAAGACGCGG
CTACTCTGTGGGGCGACGCTCATCGCCCCCAGATGGCTCCTGACAGCAGCCC
ACTGCCTCAAGCCCCGCTACATAGTTCACCTGGGGCAGCACAACCTCCAGAA
GGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAGTCCTTCCCCCACCCC
GGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATGCTGG
TGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCCTC
TCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAG
CACGTCCAGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCA
CCATCATTGAGCACCAGAAGTGTGAGAACGCCTACCCCGGCA
ACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGGACTC
CTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCA
TTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTAC

ACATCACAGACACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAGGACTC
CTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTTCAAGGCA
TTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTAC
ACGAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATT
AGACTGGACCCACCCACCACAGCCCATCACCCTCCATTTCCACTTGGTGTTTG
GTTCCTGTTCACTCTGTTAATAAGAAACCCTAAGCCAAGACCCTCTACGAACA
TTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATCAACCTGG
GGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTTGAAATATTGTGACT
CTGGGAATGACAACAC

SEQ ID NO:4

MQRLRWLRDWKSSGRGLTAAKEPGARSSPLQAMRILQLILLALATGLVGGETRII

KGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHCLKPRYIVHLGQHNL

QKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAVRPLTLS

SRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIEHQKCENAYPGNITDTMVC

ASVQEGGKDSCQGDSGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVD

WIQETMKN